An international breeding program in spring canola

Wallace Cowling

Kadambot Siddique, Jasenka Vuksic and Rozlyn Ezzy,
The University of Western Australia and NPZ Australia Pty Ltd

Olaf Sass, Sophie König and Kim Ehrlich, NPZ Lembke, Germany

Janice Duguid, Evan Gillis and Stephen Fox, DL Seeds, Canada

Inga Tetzner, DSV, Germany

An international canola breeding program

40 diverse founder lines:

Canada, Europe:	20 founders
Australia:	20 founders

Rapid $S_{0:1}$ recurrent selection (2 year cycles):

Cycle	Year	Sites
1	2014	AU1
2	2016	AU1, AU2
3	2018	CA1, AU1

BLUP analysis across cycles with optimal contributions selection based on an economic index ($/ha)

<u>Outcome</u>: high rate of genetic improvement in all traits in index

International breeding trial: Australia

York, Western Australia

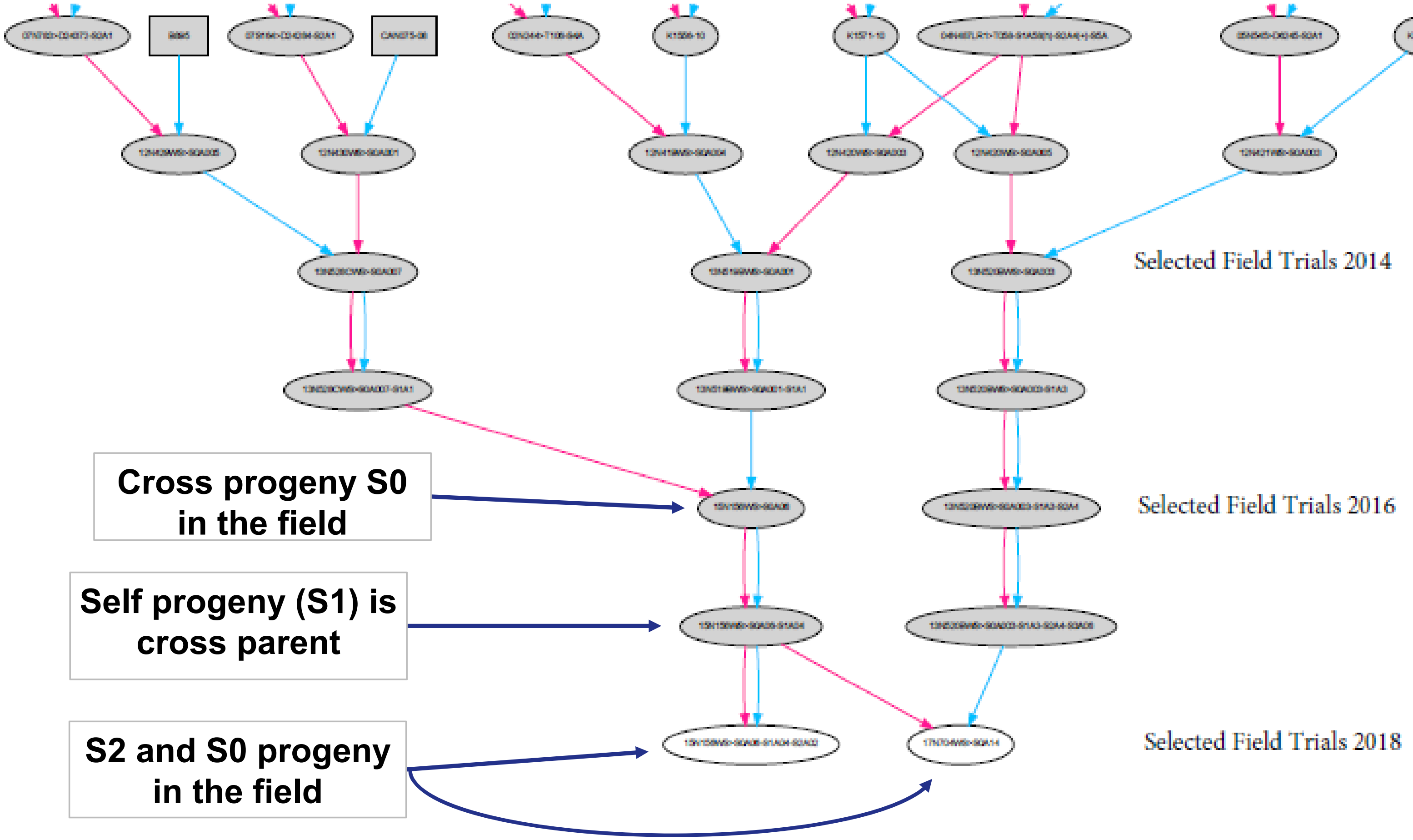
short days, winter-spring growing season

International breeding trial: Canada

Sun Valley, Manitoba

long days, summer growing season

An integrated BLUP breeding model for selfing crops



Selected Field Trials 2014

Selected Field Trials 2016

Selected Field Trials 2018

Cross progeny S0 in the field

Self progeny (S1) is cross parent

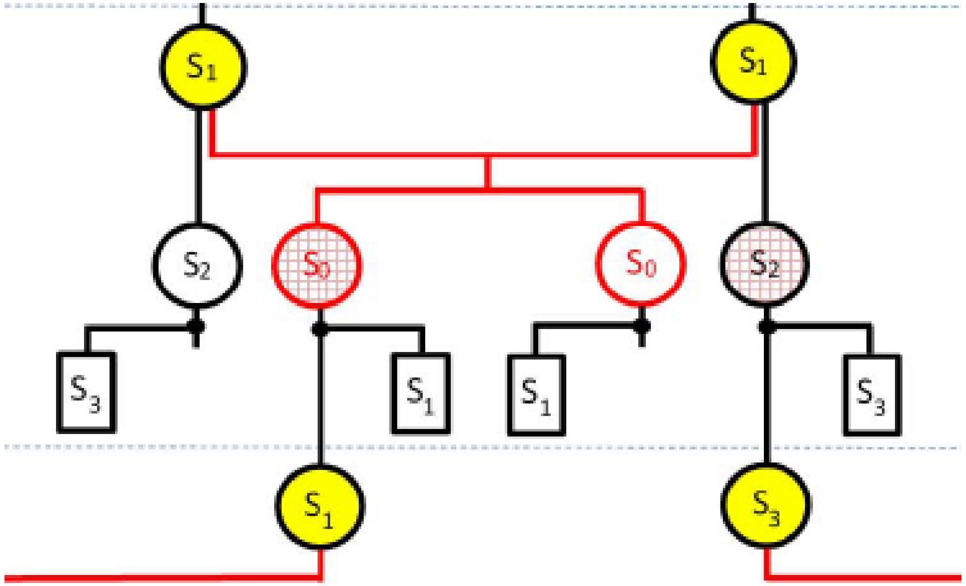
S2 and S0 progeny in the field

Cowling et al (2017) Journal of Experimental Botany 68:1927–1939.

An integrated BLUP breeding model for selfing crops

Integrate pedigree and genomic information, exploiting close relationships including selfing and crossing, with high accuracy of selection index.

The system as used in canola:



Cowling et al (2019) Food and Energy Security 8:e00157

Optimising the breeders equation for rapid international canola breeding

$$R = \frac{i r \sigma_A}{L}$$

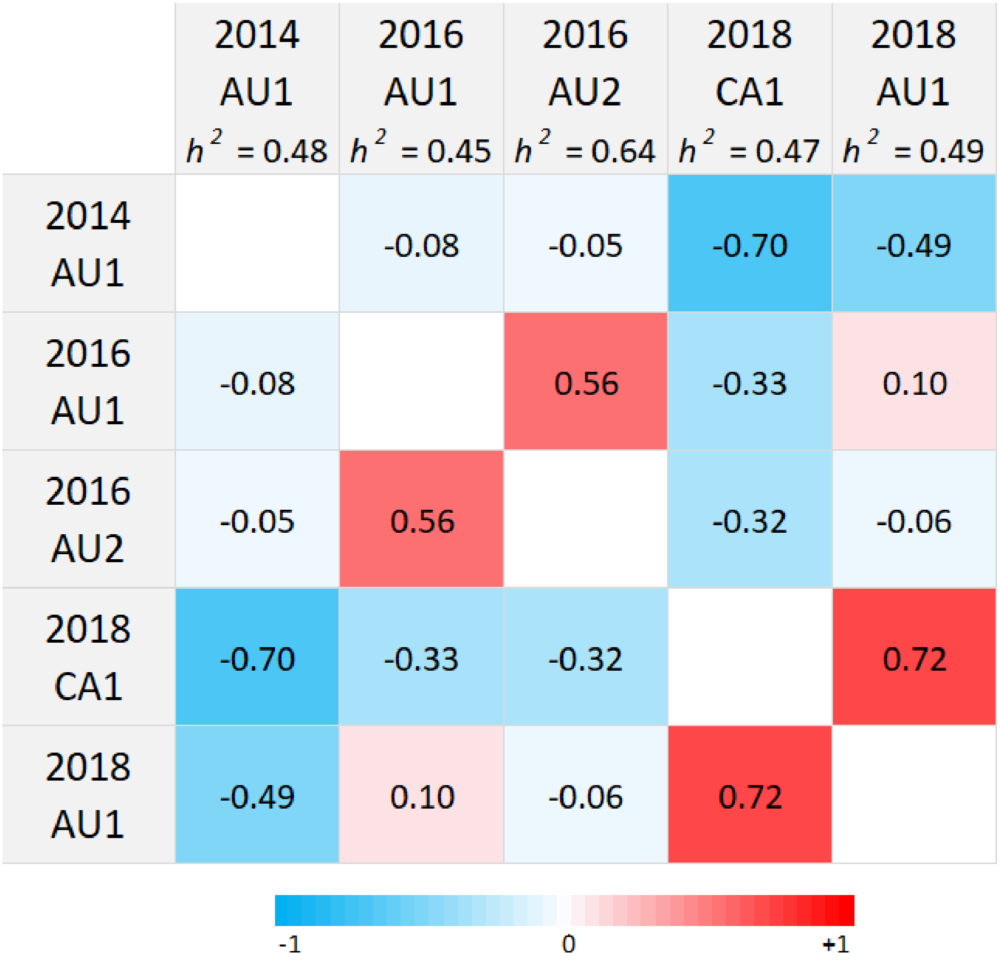
R	response to selection	(economic index \$/ha)
i	intensity of selection	(moderate)
r	accuracy of selection	(pedigree and/or genomic information)
σ_A	additive genetic variation	(diverse population)
L	is the length of cycles	(2 years biological limit)

ASREML: BLUP analysis for grain yield
(across 3 cycles 2014-2016-2018)

Variance model	Loglik	
Diagonal model:		
base model	3939.3	variety **
+ pedigree	4813.0	additive ***
+ pedigree, spatial	4944.5	additive ***
General correlation model, heterogeneous variance (corgh)		
+ pedigree, spatial	5043.4	additive*** correlations***

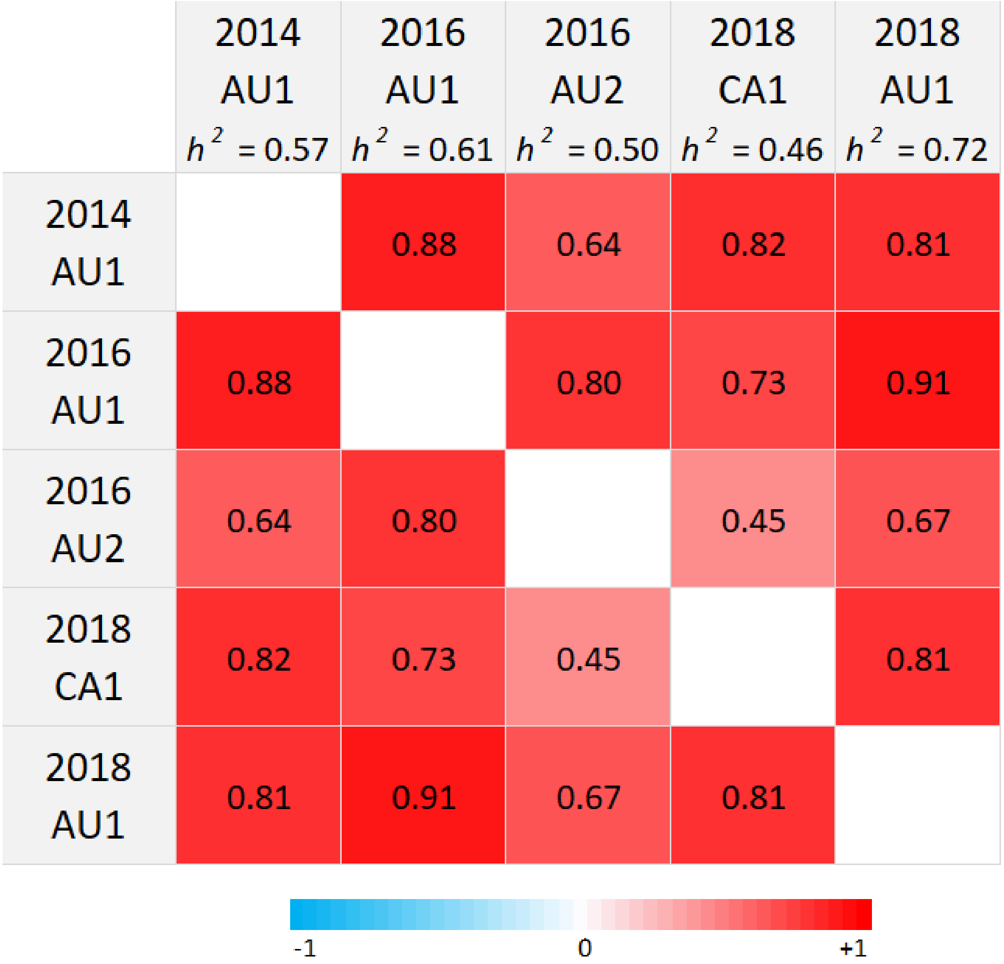
Output: predicted (estimated) breeding value (EBV) for grain yield at each site in 2014, 2016, 2018

Genetic correlations (EBV) across cycles: grain yield (t/ha)



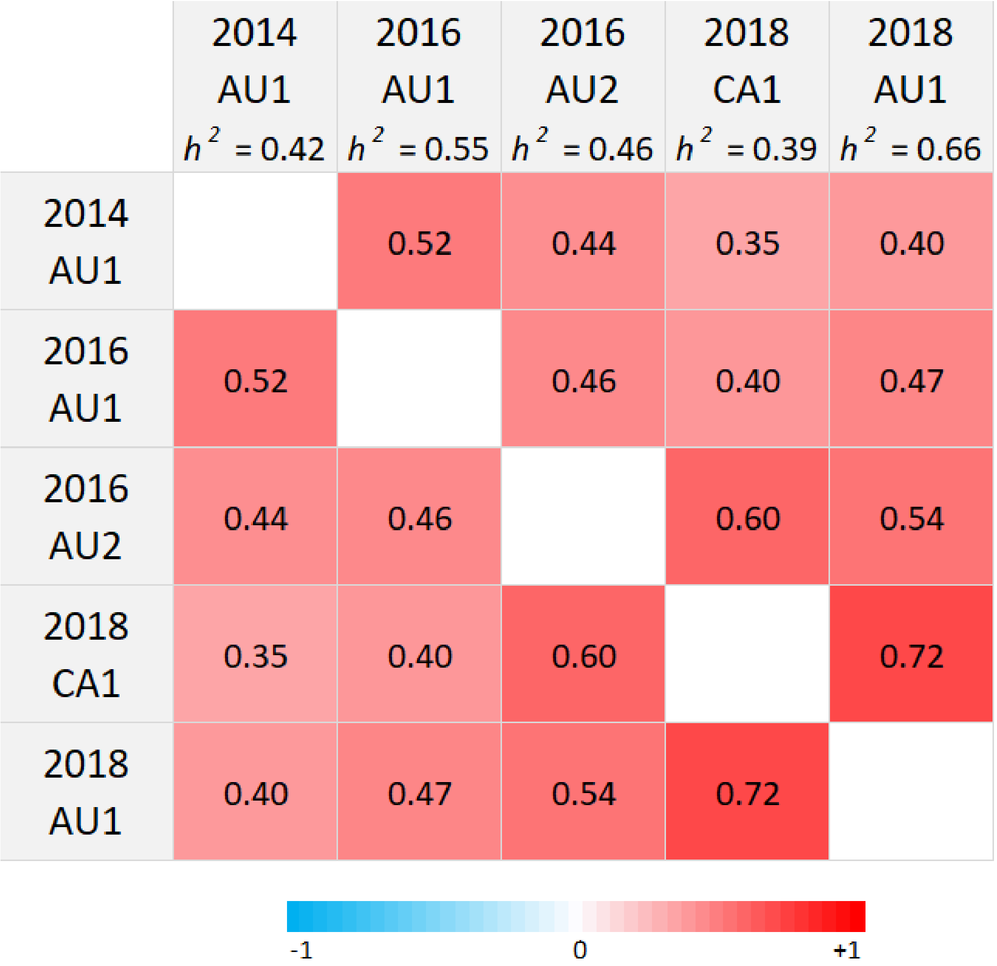
	2014 AU1 $h^2 = 0.48$	2016 AU1 $h^2 = 0.45$	2016 AU2 $h^2 = 0.64$	2018 CA1 $h^2 = 0.47$	2018 AU1 $h^2 = 0.49$
2014 AU1		-0.08	-0.05	-0.70	-0.49
2016 AU1	-0.08		0.56	-0.33	0.10
2016 AU2	-0.05	0.56		-0.32	-0.06
2018 CA1	-0.70	-0.33	-0.32		0.72
2018 AU1	-0.49	0.10	-0.06	0.72	

Genetic correlations (EBV) across cycles seed oil (%)



	2014 AU1 $h^2 = 0.57$	2016 AU1 $h^2 = 0.61$	2016 AU2 $h^2 = 0.50$	2018 CA1 $h^2 = 0.46$	2018 AU1 $h^2 = 0.72$
2014 AU1		0.88	0.64	0.82	0.81
2016 AU1	0.88		0.80	0.73	0.91
2016 AU2	0.64	0.80		0.45	0.67
2018 CA1	0.82	0.73	0.45		0.81
2018 AU1	0.81	0.91	0.67	0.81	

Genetic correlations (EBV) across cycles protein in meal (%)



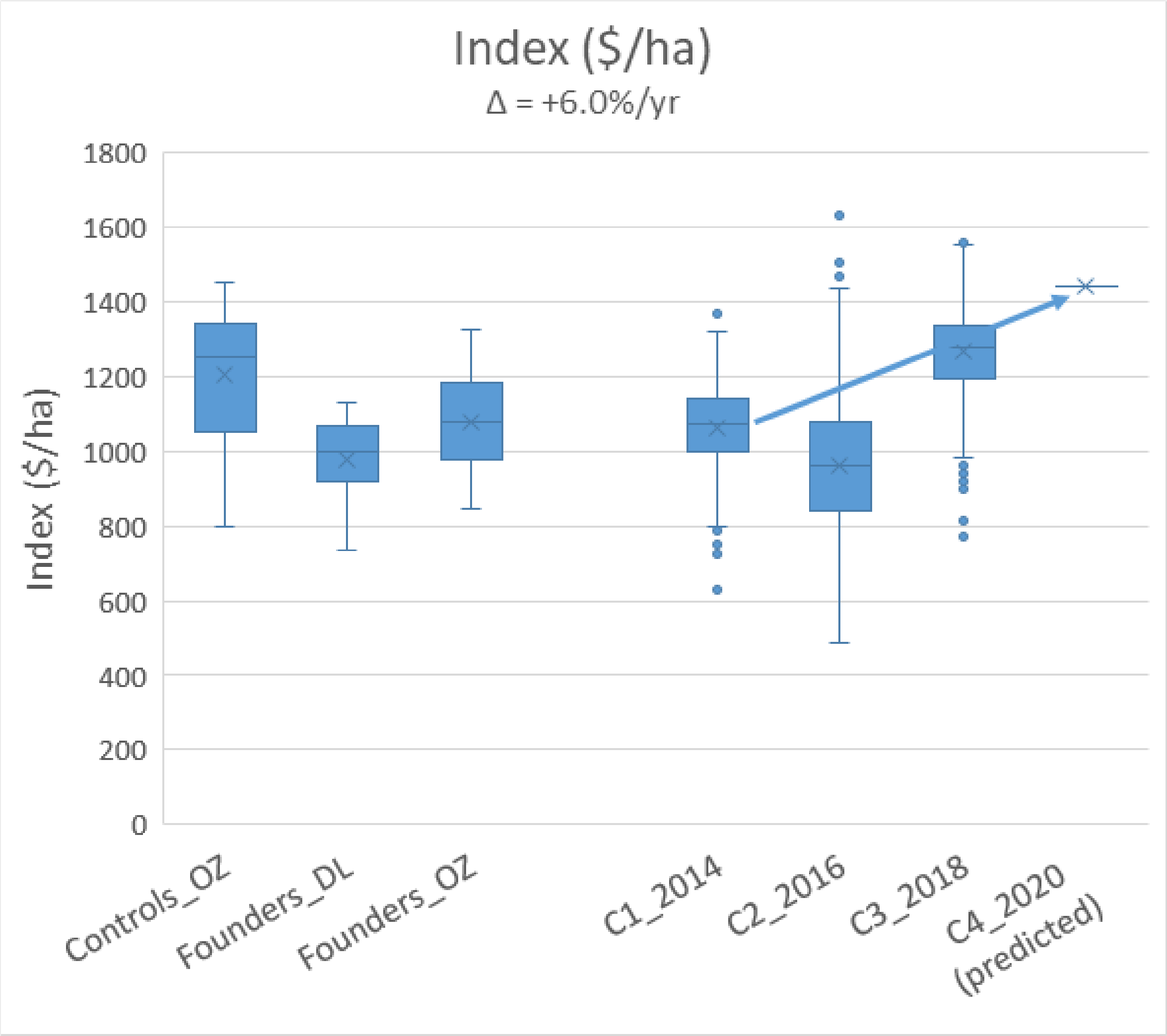
	2014 AU1 $h^2 = 0.42$	2016 AU1 $h^2 = 0.55$	2016 AU2 $h^2 = 0.46$	2018 CA1 $h^2 = 0.39$	2018 AU1 $h^2 = 0.66$
2014 AU1		0.52	0.44	0.35	0.40
2016 AU1	0.52		0.46	0.40	0.47
2016 AU2	0.44	0.46		0.60	0.54
2018 CA1	0.35	0.40	0.60		0.72
2018 AU1	0.40	0.47	0.54	0.72	

Selection in an economic index

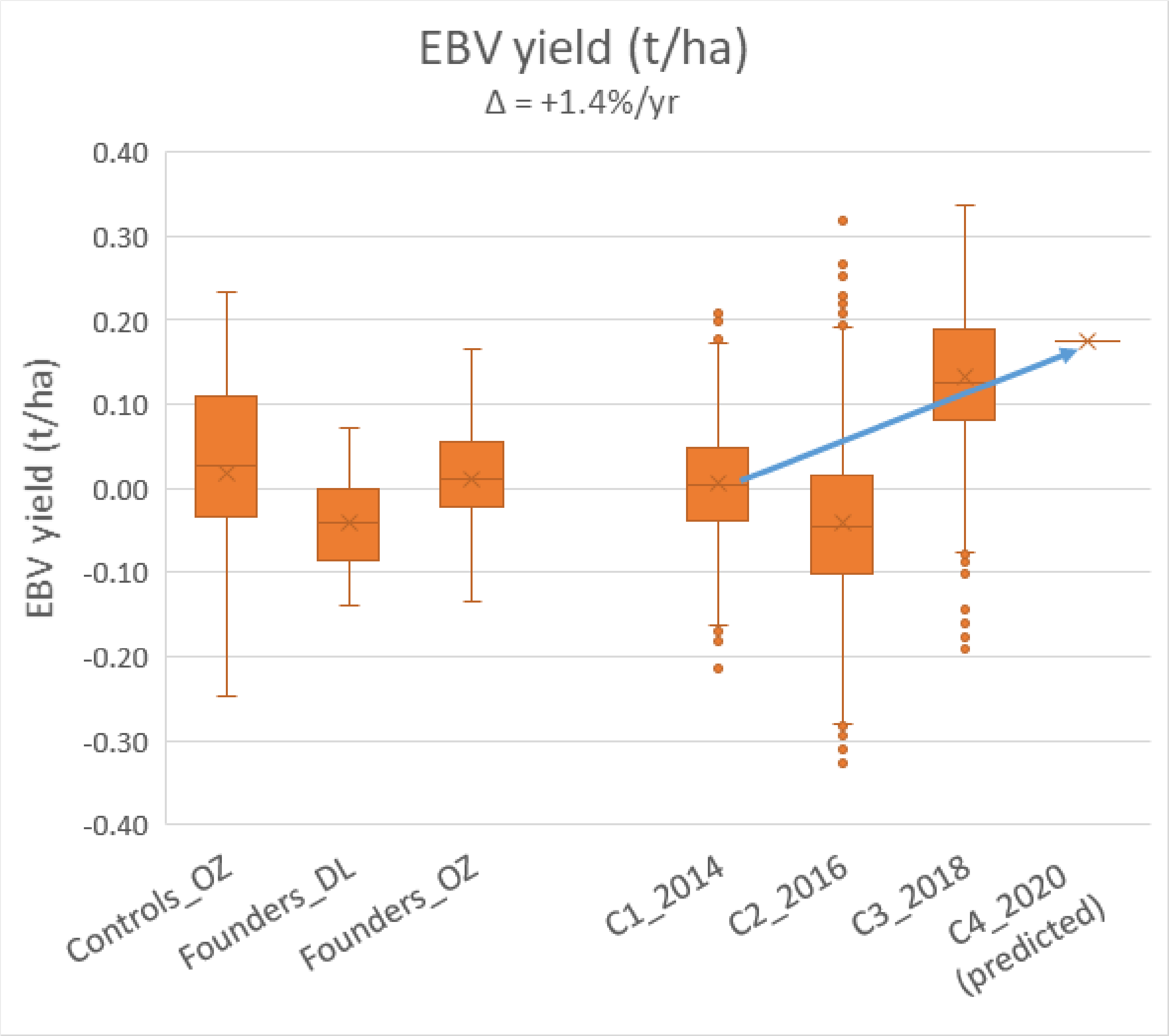
$$Index\ (\$/\mathrm{ha}) = \Sigma \quad \{\mathrm{EBV}_{\mathrm{i}} \ \times \ \textit{economic weight}\}$$

GY	EBV grain yield (t/ha)	($/ha)
$+\ DTF$	EBV days to 50% flower	× weight ($/ha)
$+\ Ht$	EBV height @ maturity	× weight ($/ha)
$+\ BL$	EBV blackleg (Phoma)	× weight ($/ha)
$+\ Oil$	EBV oil in seed (%)	× weight ($/ha)
$+\ ProM$	EBV protein in meal (%)	× weight ($/ha)
$+\ GSL$	EBV glucosinolates meal	× weight ($/ha)

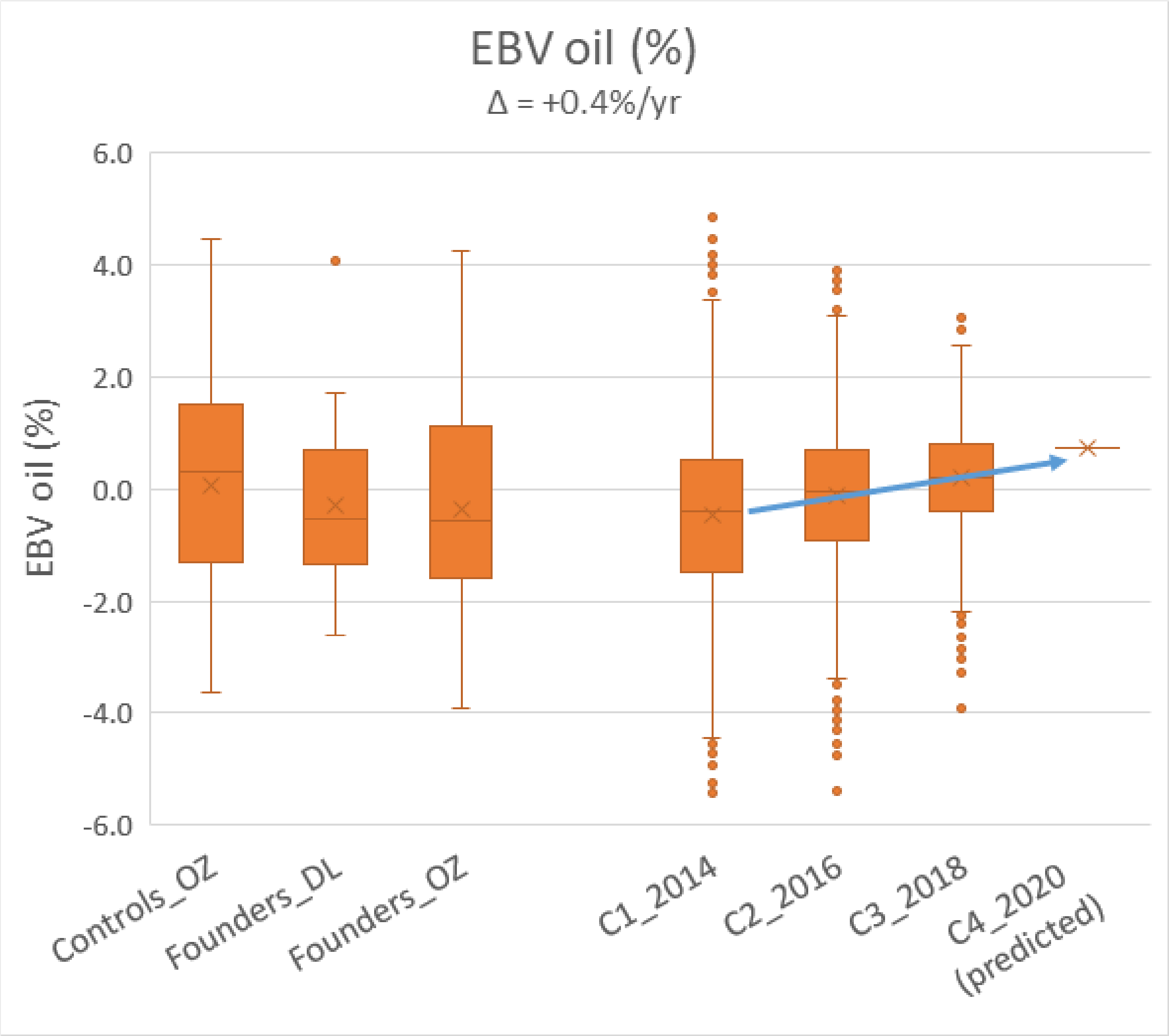
Genetic progress (R) across cycles - index ($/ha)



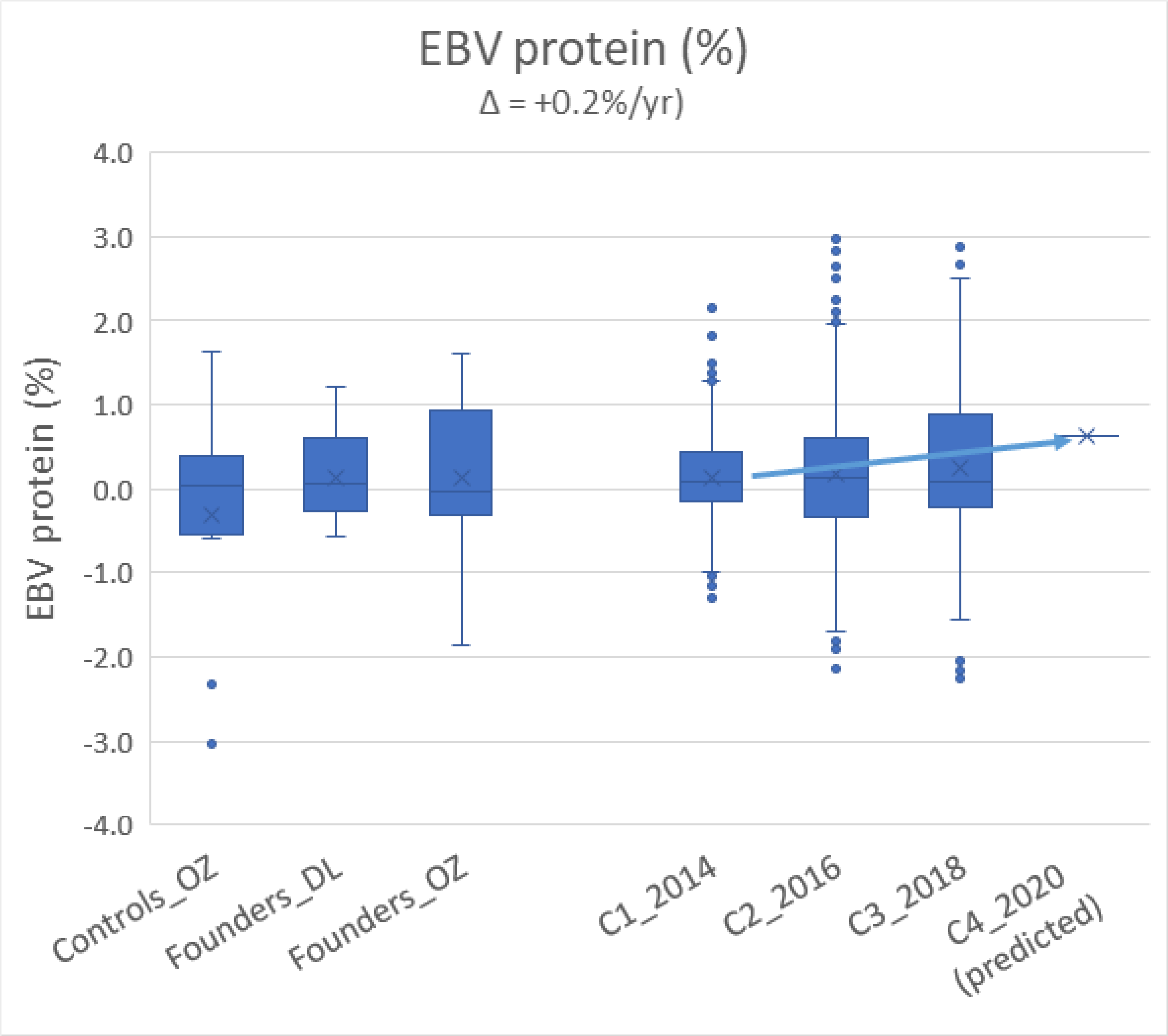
Genetic progress (R) across cycles
- grain yield (mean 1.99 t/ha)



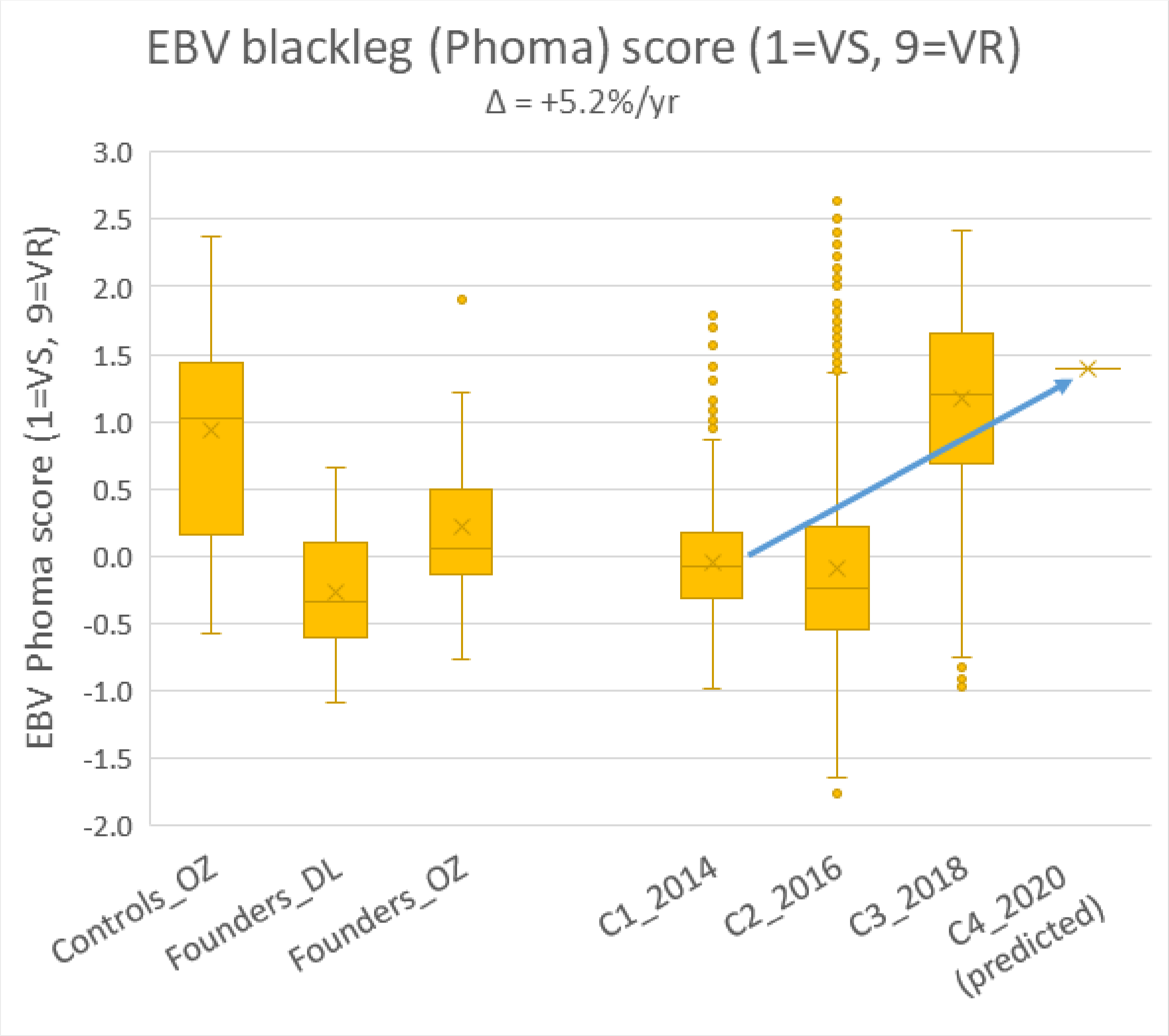
Genetic progress (R) across cycles
- seed oil (mean 46.2%)



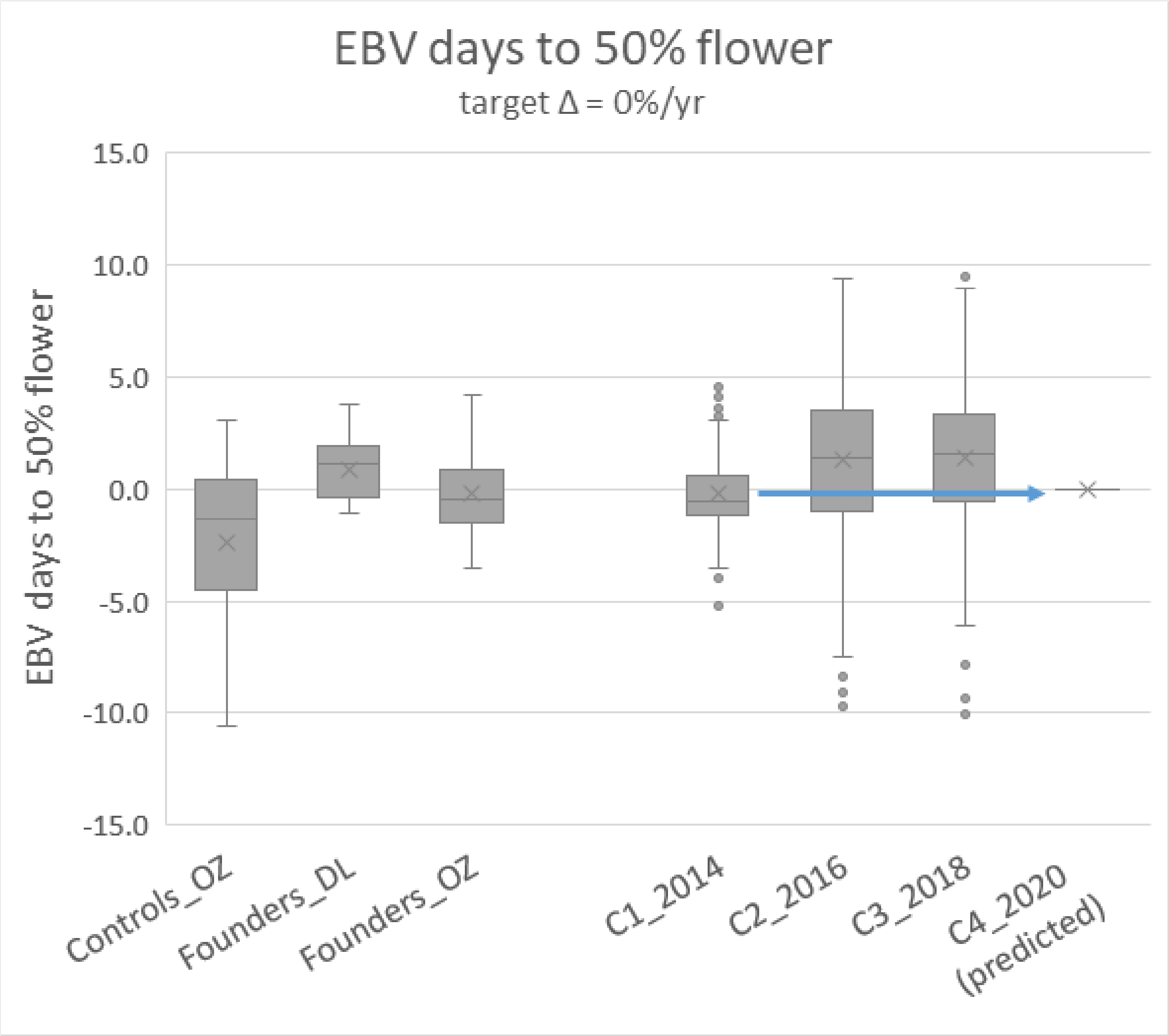
Genetic progress (R) across cycles - protein in meal (mean 43.3%)



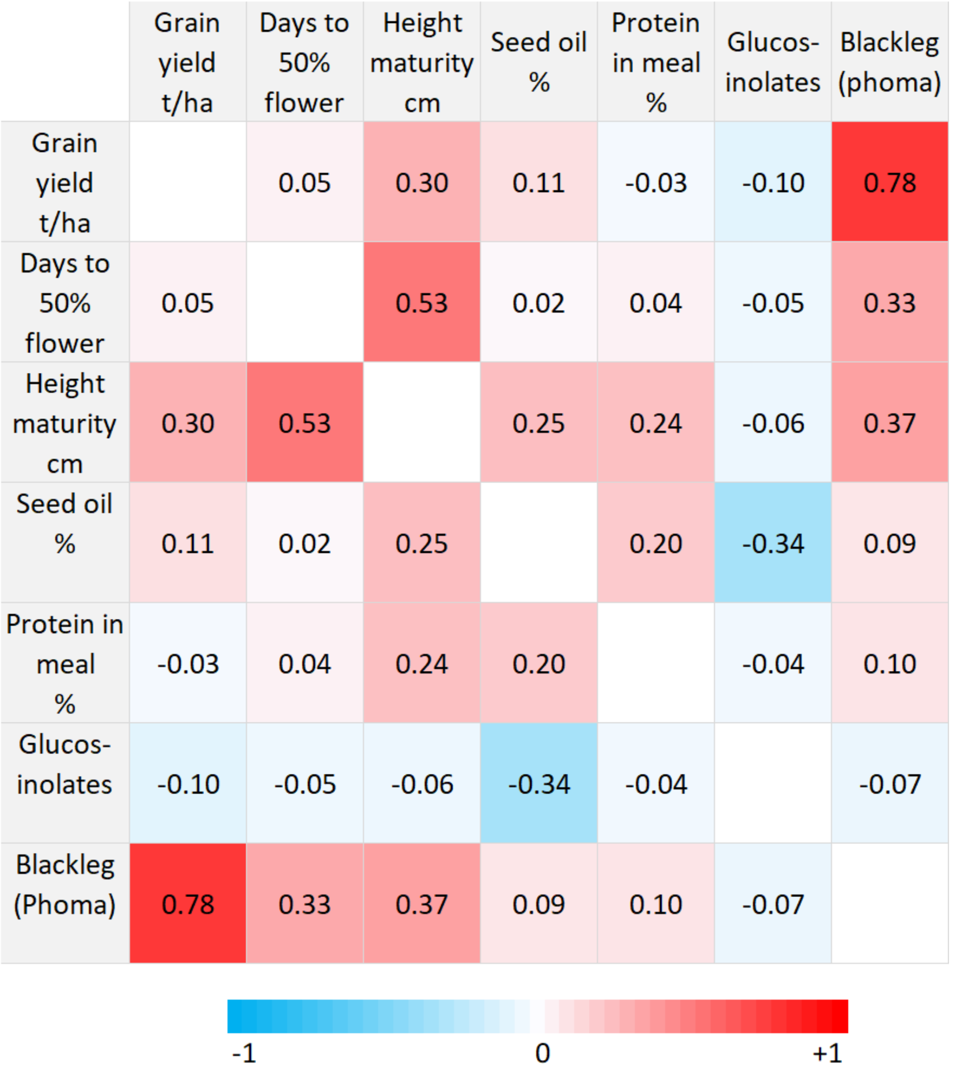
Genetic progress (R) across cycles
- blackleg disease resistance (mean = 4.6)



Genetic progress (R) across cycles
- days to 50% flower (mean 85.4 days)

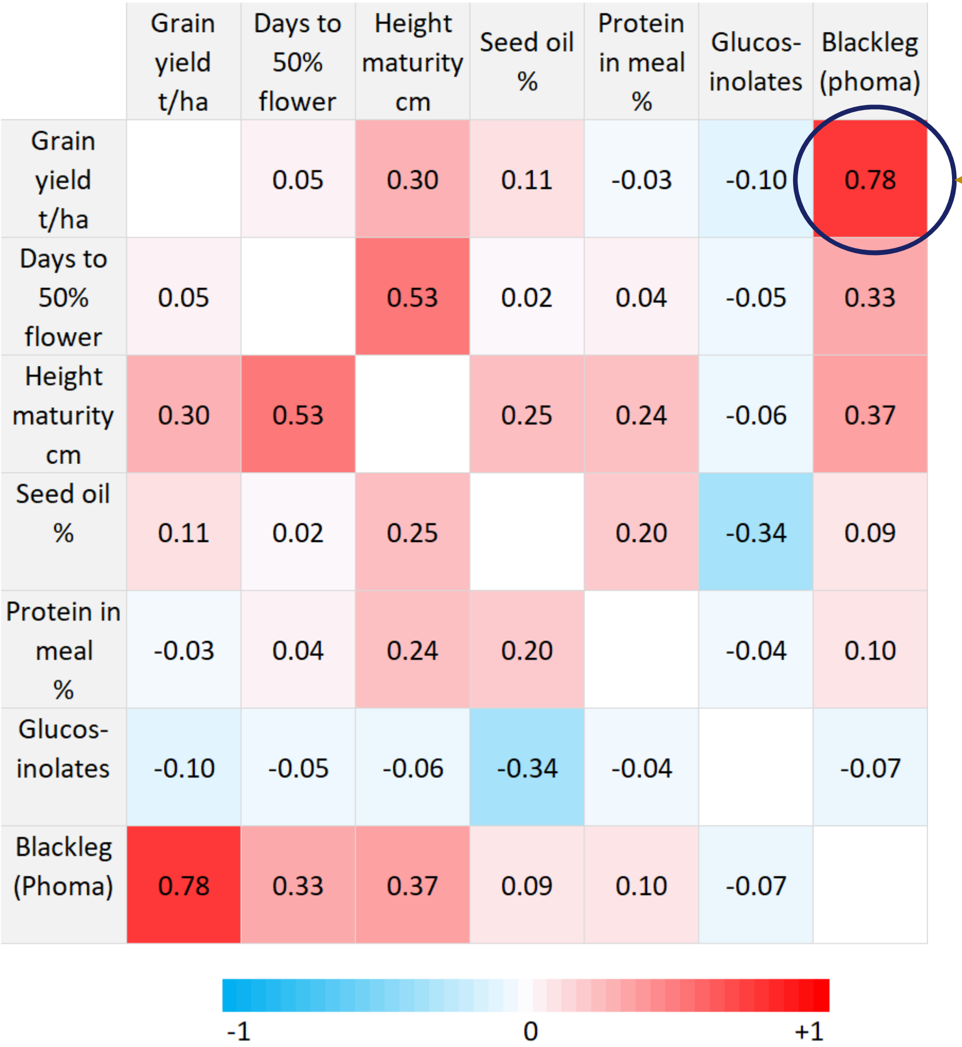


Genetic correlations (EBV) across traits



	Grain yield t/ha	Days to 50% flower	Height maturity cm	Seed oil %	Protein in meal %	Glucos-inolates	Blackleg (phoma)
Grain yield t/ha		0.05	0.30	0.11	-0.03	-0.10	0.78
Days to 50% flower	0.05		0.53	0.02	0.04	-0.05	0.33
Height maturity cm	0.30	0.53		0.25	0.24	-0.06	0.37
Seed oil %	0.11	0.02	0.25		0.20	-0.34	0.09
Protein in meal %	-0.03	0.04	0.24	0.20		-0.04	0.10
Glucos-inolates	-0.10	-0.05	-0.06	-0.34	-0.04		-0.07
Blackleg (Phoma)	0.78	0.33	0.37	0.09	0.10	-0.07	

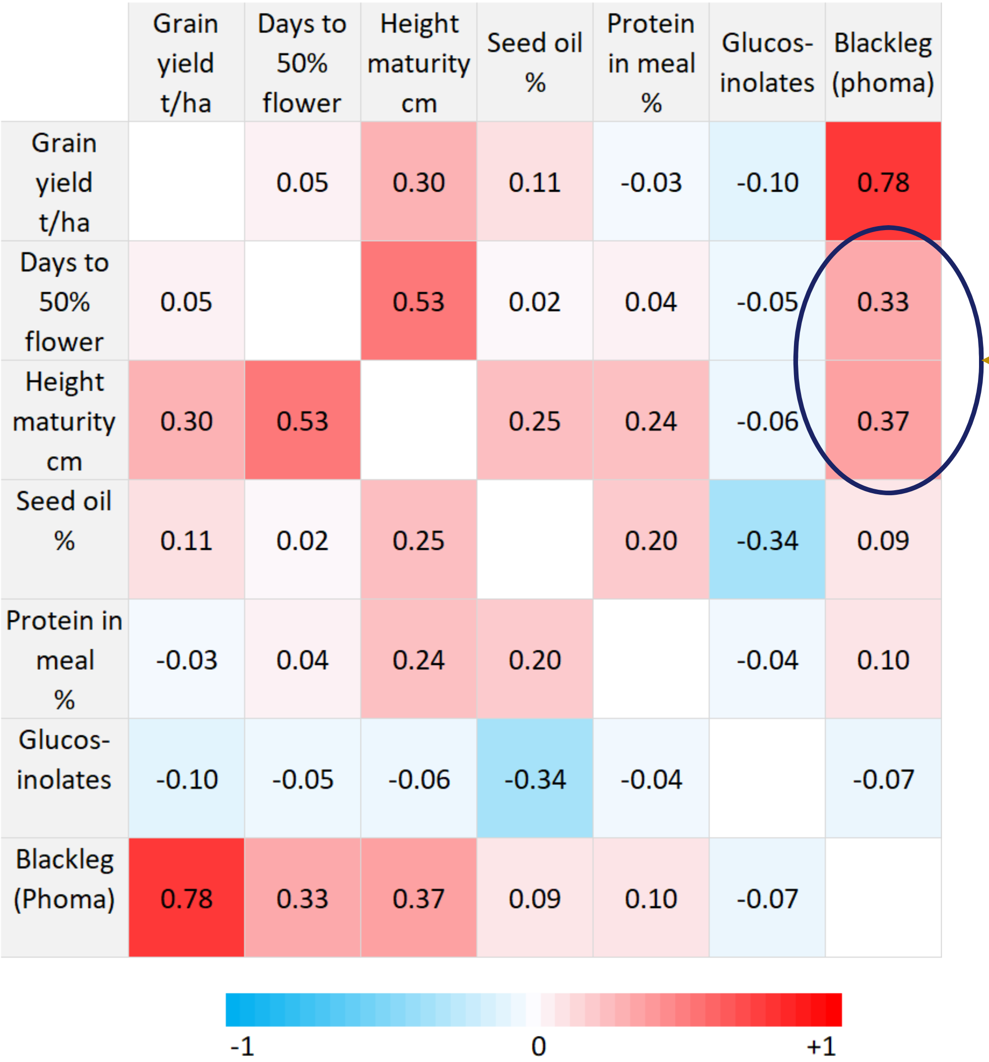
Genetic correlations across average EBV traits



	Grain yield t/ha	Days to 50% flower	Height maturity cm	Seed oil %	Protein in meal %	Glucos-inolates	Blackleg (phoma)
Grain yield t/ha		0.05	0.30	0.11	-0.03	-0.10	0.78
Days to 50% flower	0.05		0.53	0.02	0.04	-0.05	0.33
Height maturity cm	0.30	0.53		0.25	0.24	-0.06	0.37
Seed oil %	0.11	0.02	0.25		0.20	-0.34	0.09
Protein in meal %	-0.03	0.04	0.24	0.20		-0.04	0.10
Glucos-inolates	-0.10	-0.05	-0.06	-0.34	-0.04		-0.07
Blackleg (Phoma)	0.78	0.33	0.37	0.09	0.10	-0.07	

GY increases with BL resistance

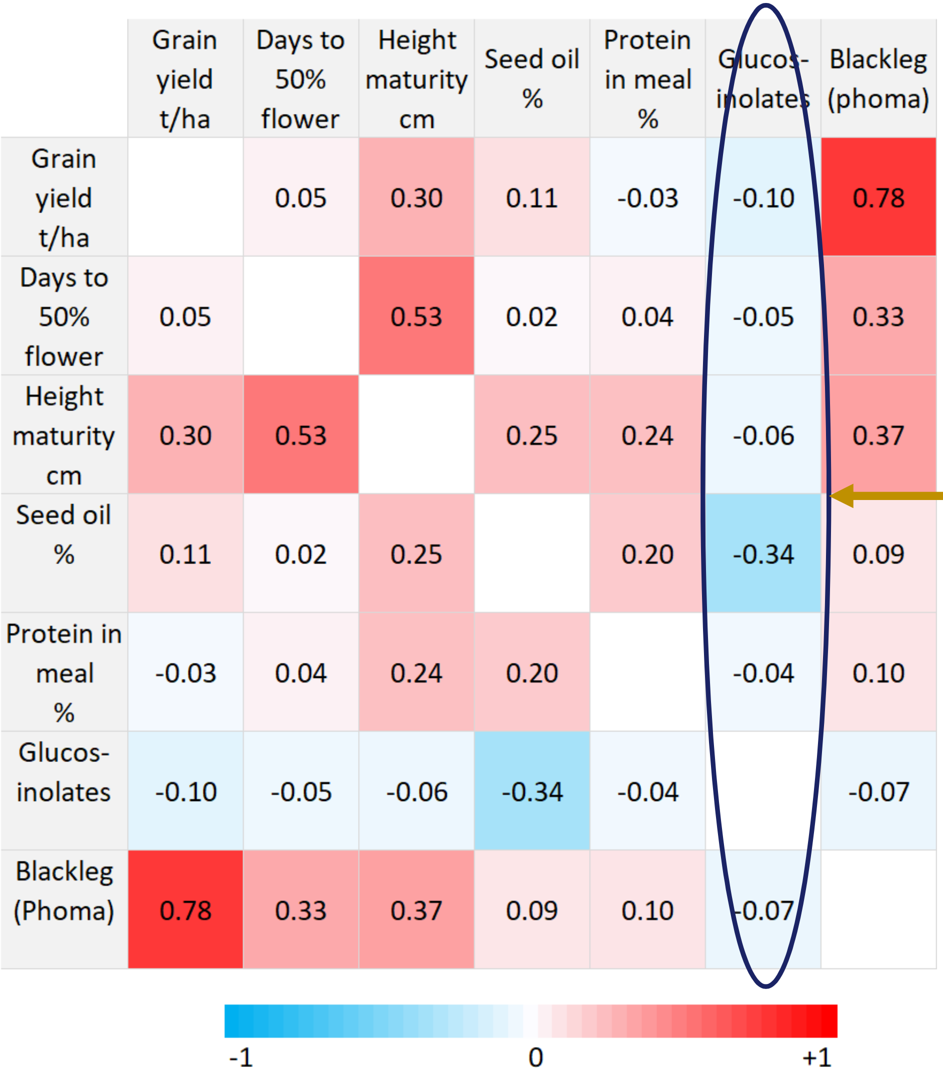
Genetic correlations across average EBV traits



	Grain yield t/ha	Days to 50% flower	Height maturity cm	Seed oil %	Protein in meal %	Glucos-inolates	Blackleg (phoma)
Grain yield t/ha		0.05	0.30	0.11	-0.03	-0.10	0.78
Days to 50% flower	0.05		0.53	0.02	0.04	-0.05	0.33
Height maturity cm	0.30	0.53		0.25	0.24	-0.06	0.37
Seed oil %	0.11	0.02	0.25		0.20	-0.34	0.09
Protein in meal %	-0.03	0.04	0.24	0.20		-0.04	0.10
Glucos-inolates	-0.10	-0.05	-0.06	-0.34	-0.04		-0.07
Blackleg (Phoma)	0.78	0.33	0.37	0.09	0.10	-0.07	

BL resistance is higher in taller and later types

Genetic correlations across average EBV traits



	Grain yield t/ha	Days to 50% flower	Height maturity cm	Seed oil %	Protein in meal %	Glucos-inolates	Blackleg (phoma)
Grain yield t/ha		0.05	0.30	0.11	-0.03	-0.10	0.78
Days to 50% flower	0.05		0.53	0.02	0.04	-0.05	0.33
Height maturity cm	0.30	0.53		0.25	0.24	-0.06	0.37
Seed oil %	0.11	0.02	0.25		0.20	-0.34	0.09
Protein in meal %	-0.03	0.04	0.24	0.20		-0.04	0.10
Glucos-inolates	-0.10	-0.05	-0.06	-0.34	-0.04		-0.07
Blackleg (Phoma)	0.78	0.33	0.37	0.09	0.10	-0.07	

High glucosinolates associated with lower GY, BL, oil, and protein in shorter and earlier types

Conclusions – international canola breeding

Valuable genetic diversity ex founders (CA, EU, AU)

Optimised mating design predicts:

- +6% per year increase in index ($/ha)
- +1.4% per year increase in grain yield (t/ha)
- +0.4% per year increase in seed oil (%)
- +0.2% per year increase in protein in meal (%)
- +5.2% per year improvement in blackleg rating

COST over 3 cycles:

- cost of phenotyping = 8,000 plots per cycle (2 years)
- 2.8 FTE staff members (field, glasshouse, database)

An international breeding program in spring canola

THANK YOU!!

IRC2023

16th INTERNATIONAL RAPESEED CONGRESS | SYDNEY
24-27 September 2023 | International Convention Centre

www.irc2023sydney.com

GCIRC
GROUPE·CONSULTATIF·INTERNATIONAL·DE·RECHERCHE·SUR·LE·COLZA


NPZ